

Repertoire determination of a lymphocyte B population

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Abstract:

The present invention provides a process for determining the quantitative and qualitative profile of the repertoire of a given type of an immunoglobulin (Ig) heavy chain expressed by a lymphocyte B population present in a tissue sample, and kits and uses thereof. It also provides a set of VH forward primers 10 associated with a CH reverse primer, which are respectively capable of specifically hybridizing in stringent conditions with the nucleic acids encoding the variable segments of Ig heavy chains and with the constant segment of a given type of Ig heavy chain, such as preferably IgM, IgG, IgE or IgA heavy chain. Methods for the *in vitro* diagnosis of a condition associated with an 15 abnormal expression of the repertoire of a given type of Ig heavy chain, and for the *in vitro* follow-up of a treatment of such a condition, are also comprised herein.

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